GenCore version Copyright (c) 1993 - 2000

nucleic search, using sw model

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Run on:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

08-09-665-363-6

Title: Perfect score: Sequence:

Scoring table:

earched:

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AR131263 Sequence
U38964 Human PMS2
AR131251 Sequence
R131251 Sequence
U14558 Human DNA m
AR141718 Sequence
U1369 Human Dmool
G18338 SWSS2476 Er
U28724 Mus musculu
D38438 Homo sapien
D38500 Human PMS6
E11279 Human CDNA
U3898 Human PMS6
U3898 Human PMS6
                                                                      AB017007 Homo sapi
D38436 Homo sapien
D38502 Human PMS4
                                                    AB017005 Homo sapi
                                                                                                                              E11277 Human cDNA
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D38499 Human PMS3
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AB017004 Homo sapi
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D38498 Human PMS5
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U38979 Human PMS2
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AC004878 Homo sapi
AC006014 Homo sapi
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Mammaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The human PMS2L proteins do not interact with hMLH1, a major mismatch repair protein
J. Blochem. 125 (41, 818-825 (1999)
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AC007000 F
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Homo sapiens PMS2L14 mRNA, partial cds.
AB017005.1 GI:4239951
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Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

sapi sapi sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_htgo\_inv:\*
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110... 112... 112... 114... 116... 122... 122... 122... 122... 122... 122... 123... 124... 125... 126... 127... 127... 127...

em\_fun:\*

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gb\_sy:\*

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gb\_htg:\*

gb\_ba:\* GenEmbl:\*

Database

gb\_in:\* gb\_om:\*

em\_htg\_other:\*

DNA

SUMMARIES

2 (bases 1 to 1096) Horii,A. Direct Submission

REFERENCE AUTHORS TITLE

J. Biochem.

JOURNAL MEDLINE

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AB017007.1
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KIVGNSLDAGATNIDLKLKDYGMDLIEVSGNGCGVEEENFEGLSLSALKHHTSKIREF
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Submitted (18-AUG-1998) to the DDBJ/EMBL/GenBank databases. Aki Horii, Tohoku University School of Medicine, Department of Molecular Pathology; 2-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-117-8042, Fax:81-22-717-8047)
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/protein_id="BAA74754.1"
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cetacececaceceagaggaceacagteagegtgaageagttatttetaegetaeetg
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RESULT 2
AB017007
AB01707
AB017

Location/Qualifiers

Location/

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1 O81785 arabidopsis thaliana
1 OgrtrO deinococcus radiodura
1 Q9he21 neurospora crassa.re
1 Q12083 saccharomyces cerevis
1 Q9h1a8 homo sapiens (human).
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MEDLINE-99203588; Pubmed-10104297;
Kondo E., Horil A., Fukushige S.;
"The human PMS2L proteins do not interact with hMLH1, a major DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 ATGGGAAAATCATCCAGAAAACCCCCTACCCCCCCCCAGGGGGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetG1¶GluSerSerArgLysProProThrProThrProGluGlyProTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636 AGTCAGCGTGAAGCAGTTATTTTCTACGCTACCTGTGCGCCATAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 ITCAAAGGAATATTAAGAAGAAACGTGCCTGCTTCCCCTTCGCCTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 CGTGATTGTCAGTTTCTTGAGGGCTCCCCAGCCATGCTTCCTGTACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         786 IGCAAAACTIACAGAACCIGCIAAGGCCAICAAACCIATIGAICGGAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ValLysLysIleValGlyAsnSerLeuAspAlaGlyAlaThrAsnIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTAAAGCTTAAGGACTATGGAATGGATCTCATTGAAGTTTCAGGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAAGAAGATAGTAGGAAACAGTCTGGATGCTGGTGCCACTAATATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
SEQUENCE 297 AA; 32669 MW; 9D05D86F583B917D CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 99.663
1151
547
860
715
116
      .6e-10
.7e-09
.5e-08
.0e-07
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                                                                                                                                                                                                                                                                                                              PRT;
      318.60
296.30
281.30
259.32
265.97
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7-Riochem. 125:818-825(1999)....

EMBL; AB017005; BAA74754.1; -.
                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
211.00
193.50
186.50
172.00
167.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1552.00
Ratio: 5.226
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                           seq_documentation_block:
ID 095744 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: 095744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-665-363-6 x 095744
                                                                                                                                                                                                         seq_name: sp_human:095744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P23367; 1BKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMS2L14 PROTEIN. PMS2L14.
sp_plant:081785
sp_bacteria:09RTR0
sp_fungi:Q9HE21
sp_fungi:012083
sp_human:Q9H1A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                 Score_list:
Scrote_list:
Scrote_list:
Score_list:
Score_list:
Score_list:
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Scrote_list:
Sp.human:095744 + 1552.00 2500.56 | 18e-131 297 | 109574 homo saptiens (human). pm sp.human:091570 + 1004.50 | 1647.86 | 1.2e-78 | 389 | 101557 homo saptiens (human). pm sp.human:015630 + 965.00 1149.68 | 1.2e-78 | 389 | 101557 homo saptiens (human). pm sp.human:016630 + 965.00 1149.68 | 1.2e-78 | 389 | 1015370 homo saptiens (human). pm sp.human:016603 + 965.00 1149.68 | 1.2e-78 | 389 | 1015400 homo saptiens (human). pm sp.human:016603 + 965.00 11581.68 | 2.8e-67 | 161 | 109573 homo saptiens (human). pm sp.human:016673 + 72.00 1169.91 4.3e-57 | 161 | 101673 homo saptiens (human). pm sp.human:016673 + 537.50 | 888 59 | 2.8e-47 | 114 | 094053 homo saptiens (human). pm sp.human:01670 + 537.50 | 888 59 | 2.8e-47 | 114 | 094052 homo saptiens (human). pm sp.human:01670 + 537.50 | 888 59 | 2.8e-47 | 114 | 094052 homo saptiens (human). pm sp.human:01670 + 537.50 | 888 59 | 2.8e-47 | 114 | 094052 homo saptiens (human). pm sp.human:01670 + 466.00 774.59 | 16e-13 | 7.9e-13 | 1095746 homo saptiens (human). pm sp.human:099054 + 465.00 774.59 | 16e-13 | 7.9e-13 | 1095746 homo saptiens (human). pm sp.human:099745 + 465.00 774.59 | 16e-13 | 7.9e-13 | 1095746 homo saptiens (human). pm sp.human:099745 + 465.00 774.59 | 16e-13 | 7.9e-14 | 1095746 homo saptiens (human). pm sp.human:099745 + 465.00 774.59 | 16e-13 | 7.9e-14 | 1095746 homo saptiens (human). pm sp.human:099745 + 465.00 774.59 | 16e-13 | 7.9e-24 | 80 | 104574 homo saptiens (human). pm sp.human:090745 + 402.00 644.44 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28 | 144 | 86-28
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                                                                                                                                                                                                                          Command line parameters:
-MODEL-frame+_n2p.model -DEV-x1p
-MODEL-frame+_n2p.model -DEV-x1p
-O-<model-o2p.model -DEV-x1p
-O-<model-o2p.model -DEV-x1p
-O-<model-o2p.model -DEV-x1p
-O-<model-o2p.model-o2p.model -DEV-x1p
-O-<model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model-o2p.model
                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
             out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 4 246.00 380.29 1.10-13 46 245.50 381.75 1.20-13 46 245.50 378.18 1.20-13 46 242.50 374.12 2.20-13 65 240.50 370.82 3.30-13 72 239.00 367.55 4.60-13 73 232.50 357.92 1.80-12 66 34 2.230.50 357.22 2.70-12
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219.00 336.35 2.
      OM of: US-09-665-363-6 to: SPTREMBL_17:*
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Query length: 1658
Database: SPTREMBL_17:*
Database sequences: 473505
Database length: 146272329
Search time (sec): 142.870000
                                                                        Date: Mar 12, 2002 11:08 PM
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sp_bacteria:099XN7
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RA
DR
DR
DR
DR
SQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                           GCCATAAGGAATTTCAAAGGAATATTAAGAAGAAACGTGCCTGCTTCCCC 1335
                               1035
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                              167
                                                                                                                              uthrpheglypheglnGlyLysAlaLeuSerSerLeuCysAlaLeuSerA 184
                                                                                                                                                                                                                                                                       234
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"The sequence of Homo sapiens PAC clone DJ0953A04.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                           1336 TICGCCTICIGCCGIGALIGICAGITICITGAGGGCICCCCAGCCAIGCI
                                                                                                                                                                                                                                                                                                                                                                                 1386 TCCTGTACAGCCTGCAAAACTGACTGTAACTGGAGAGCTACGGGCATGCA
1036 AAACATCACACATCTAAGATTCGAGAGTTTGCCGACCTAACTCGGGTTGA
                                                                                                                    AACTTTTGGCCTTTCAGGGGAAAGCTCTGAGCTCACTTTGTGCACTGAGTG
                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          1436 GAAGTIGGAAGACGAAGGCAICACAGAGGCIGIGGGG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99063792; PubMed-9847074; Sulston J.E., Waterston R.; Sulston J.E., Waterston R.; Genome sequence."; Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA
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01-NOV-1999 (TrEMBLrel. 12, Last sequenc)
01-JUN-2001 (TrEMBLrel. 17, Last annota'
WUGSC:H_DJ0953A04.2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_human:09Y2N0
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09Y2N0;
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GCCGTGATTGTCAGTTTCTTGAGGCTCCCCAGCCATGCTTCCTGTACAG 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                996 AGAAGAAGAAACTTCGAAGGCTTATCTCTTTCAGCTCTGAAACATCACA 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCTAAGATTCGAGGTTTGCCGACCTAACTCGGGTTGAAACTTTTGGC 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1146 ITCTACCTGCCACGTATCGGCGAAGGTTGGGACTCGACTGGTGTTTGATC 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 isAspGlyLysIleIleGlnLysThrProTyrProH1sProArgGlyThr 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 ysargAspCysGlnPheLeuGluGlySerProAlaMetLeuProValGln 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 PheargGlyLysAlaLeuSerSerLeuCysAlaLeuSerAspValThril 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
ACO06014; AAD28062.1; --
HSSP; P23367; 1BKN.
HSSP; P23367; 1BKN.
InterPro; 1PR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
                                                                                                                                                                                                                                                                                                                                                796 ACAGAACCIGCIAAGGCCATCAAACCTAITGAICGGAAGICAGICCAICA
                                                                                                                                                                                                                                                                                                                                                                                                                   846 GATTTGCTCTGGGCCGGTGGTACTGAGTCTAAGCACTGCGGTGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                        896 TAGTAGGAAACAGTCTGGATGCTGGTGCCACTAATATTGATCTAAAGCTT
                                                                                                                                                                                                                                                                                                                                                                   23 ThrGluproAlaLysAlaIleLysProIleAspArgLysSerValHisGl
                                                                                                                 254 AA; 27442 MW; 923FE4A3002BBFC3 CRC64;
                                                                                                                                                                                  Length: 205
Gaps: 1
Percent Identity: 96.585
                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9Y2N0 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGCAAACTGACT 1410
                                                                                                                                                                           alignment_scores:
Quality: 1024.50
Ratio: 5.072
Percent Similarity: 98.537
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